

SEQUENCE LISTING

<110> Tsuji, Takashi
 Tezuka, Katsunari
 Hori, Nobuaki

<120> HUMAN MONOCLONAL ANTIBODY AGAINST A
 COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
 PHARMACEUTICAL USE THEREOF

<130> 06501-079001

<140> US 09/859,053

<141> 2001-05-16

<150> JP 2001-99508

<151> 2001-03-30

<150> JP 2000-147116

<151> 2000-05-18

<160> 43

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Artificially synthesized primer sequence, NotI-T

<221> primer_bind

<222> (1)...(45)

<400> 1

aactggaagc ttcagcggcc gcagagattt tttttttttt ttttt

45

<210> 2

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Artificially synthesized linker sequence, 20adp

<400> 2

cgtggtgtca tggcactgcg

20

<210> 3

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Artificially synthesized linker sequence, 24adp

<400> 3
aattcgcagt gccatgacac cacg 24

<210> 4
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificially synthesized primer sequence, HIGLC

<221> primer_bind
<222> (1)...(23)
<400> 4
gtctgctttg ctcagcgtca ggg 23

<210> 5
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificially synthesized primer sequence, NHCc2

<221> primer_bind
<222> (1)...(21)
<400> 5
cacccggttcg gggaagtagt c 21

<210> 6
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificially synthesized primer sequence, ExcellE

<221> primer_bind
<222> (1)...(21)
<400> 6
ggtgacacta tagaatacag g 21

<210> 7
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificially synthesized primer sequence, ck117

<221> primer_bind
<222> (1)...(25)

<400> 7
 gcaggcacac aacagaggca gttcc 25

 <210> 8
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Artificially synthesized primer sequence, M13R

 <221> primer_bind
 <222> (1)...(20)

 <400> 8
 cacaggaaac agctatgacc 20

 <210> 9
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Artificially synthesized primer sequence, 136H

 <221> primer_bind
 <222> (1)...(21)

 <400> 9
 cctggacaag ggcttgagtg g 21

 <210> 10
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Artificially synthesized primer sequence, 138/9H

 <221> primer_bind
 <222> (1)...(21)

 <400> 10
 acaggaaaag gtctggagtg g 21

 <210> 11
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Artificially synthesized primer sequence, AILIMHC1

 <221> primer_bind
 <222> (1)...(21)

 <400> 11

acagtaatac acggccgtgt c 21

<210> 12
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificially synthesized primer sequence, HCc1

<221> primer_bind
 <222> (1)...(21)

<400> 12
 gactacttcc ccgaaccggt g 21

<210> 13
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificially synthesized primer sequence, HCc7

<221> primer_bind
 <222> (1)...(22)

<400> 13
 gtggcaggac cgtcagtctt cc 22

<210> 14
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificially synthesized primer sequence, HCc8

<221> primer_bind
 <222> (1)...(24)

<400> 14
 aagaggaaga ctgacggtcc tgcc 24

<210> 15
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificially synthesized primer sequence, HCc3

<221> primer_bind
 <222> (1)...(23)

<400> 15

ccgttggtgca ccaggactgg ctg 23

<210> 16
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificially synthesized primer sequence, HCc4

<221> primer_bind
 <222> (1)...(23)

<400> 16
 tgcacttgta ctcccttgccg ttc 23

<210> 17
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificially synthesized primer sequence, HCc6

<221> primer_bind
 <222> (1)...(23)

<400> 17
 cagccggaga acaactacaa gac 23

<210> 18
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificially synthesized primer sequence, HIGHC

<221> primer_bind
 <222> (1)...(22)

<400> 18
 tcttgtagtt gttctccggc tg 22

<210> 19
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificially synthesized primer sequence, HCc9

<221> primer_bind
 <222> (1)...(22)

<400> 19
 tacttcccag gcaccagca tg 22

<210> 20
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificially synthesized primer sequence, HCC5

<221> primer_bind
 <222> (1)...(23)

<400> 20
 atgctgggtg cctgggaagt atg

23

<210> 21
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificially synthesized primer sequence, polyA

<221> primer_bind
 <222> (1)...(21)

<400> 21
 tcaaactatc ggccttgctg g

21

<210> 22
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificially synthesized primer sequence, AILIMLC1

<221> primer_bind
 <222> (1)...(21)

<400> 22
 tagcctggta tcagcagaaa c

21

<210> 23
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificially synthesized primer sequence, AILIMLC2

<221> primer_bind
 <222> (1)...(21)

<400> 23
 gtttctgctg ataccaggct a

21

<210> 24
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificially synthesized primer sequence, LCc1

<221> primer_bind
 <222> (1)...(22)

<400> 24
 gcaccatctg tcttcatctt cc 22

<210> 25
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificially synthesized primer sequence, LCc2

<221> primer_bind
 <222> (1)...(21)

<400> 25
 caaagagctt caacagggga g 21

<210> 26
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificially synthesized primer sequence, HIK

<221> primer_bind
 <222> (1)...(20)

<400> 26
 aggctggaac tgaggagcag 20

<210> 27
 <211> 1616
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> (1)...(68)

<221> CDS
 <222> (69)...(1478)

<221> 3'UTR
 <222> (1482)...(1616)

<221> sig_peptide

<222> (69)...(125)

<400> 27

gaattcgag tgccatgaca ccacgcatct gtccctctaga gaatcccctg agagctccgt 60

tcctcacc atg gac tgg acc tgg agg atc ctc ttc ttg gtg gca gca gcc 110

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala

-15

-10

aca gga gcc cac tcc cag gtg cag ctg gtg cag tct ggg gct gag gtg 158

Thr Gly Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val

-5

1

5

10

aag aag cct ggg gcc tca gtg aag gtc tcc tgc aag gct tct gga tac 206

Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr

15

20

25

acc ttc acc ggc tac tat atg cac tgg gtg cga cag gcc cct gga caa 254

Thr Phe Thr Gly Tyr Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln

30

35

40

ggg ctt gag tgg atg gga tgg atc aac cct cac agt ggt ggc aca aac 302

Gly Leu Glu Trp Met Gly Trp Ile Asn Pro His Ser Gly Gly Thr Asn

45

50

55

tat gca cag aag ttt cag ggc agg gtc acc atg acc agg gac acg tcc 350

Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser

60

65

70

75

atc agc aca gcc tac atg gag ctg agc agg ctg aga tcc gac gac acg 398

Ile Ser Thr Ala Tyr Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr

80

85

90

gcc gtg tat tac tgt gcg agg acg tat tac tat gat agt agt ggt tat 446

Ala Val Tyr Tyr Cys Ala Arg Thr Tyr Tyr Tyr Asp Ser Ser Gly Tyr

95

100

105

tac cat gat gct ttt gat atc tgg ggc caa ggg aca atg gtc acc gtc 494

Tyr His Asp Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val

110

115

120

tct tca gcc tcc acc aag ggc cca tcg gtc ttc ccc ctg gcg ccc tgc 542

Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys

125

130

135

tcc agg agc acc tcc gag agc aca gcg gcc ctg ggc tgc ctg gtc aag 590

Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys

140

145

150

155

gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg aac tca ggc gct ctg 638

Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu

160

165

170

acc agc ggc gtg cac acc ttc cca gct gtc cta cag tcc tca gga ctc 686

Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu

175

180

185

tac tcc ctc agc agc gtg gtg acc gtg ccc tcc agc aac ttc ggc acc	734
Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr	
190 195 200	
cag acc tac acc tgc aac gta gat cac aag ccc agc aac acc aag gtg	782
Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val	
205 210 215	
gac aag aca gtt gag cgc aaa tgt tgt gtc gag tgc cca ccg tgc cca	830
Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro	
220 225 230 235	
gca cca cct gtg gca gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc	878
Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro	
240 245 250	
aag gac acc ctc atg atc tcc cgg acc cct gag gtc acg tgc gtg gtg	926
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val	
255 260 265	
gtg gac gtg agc cac gaa gac ccc gag gtc cag ttc aac tgg tac gtg	974
Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val	
270 275 280	
gac ggc gtg gag gtg cat aat gcc aag aca aag cca cgg gag gag cag	1022
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln	
285 290 295	
ttc aac agc acg ttc cgt gtg gtc agc gtc ctc acc gtt gtg cac cag	1070
Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln	
300 305 310 315	
gac tgg ctg aac ggc aag gag tac aag tgc aag gtc tcc aac aaa ggc	1118
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly	
320 325 330	
ctc cca gcc ccc atc gag aaa acc atc tcc aaa acc aaa ggg cag ccc	1166
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro	
335 340 345	
cga gaa cca cag gtg tac acc ctg ccc cca tcc cgg gag gag atg acc	1214
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr	
350 355 360	
aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tac ccc agc	1262
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser	
365 370 375	
gac atc gcc gtg gag tgg gag agc aat ggg cag ccg gag aac aac tac	1310
Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr	
380 385 390 395	
aag acc aca cct ccc atg ctg gac tcc gac ggc tcc ttc ttc ctc tac	1358
Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr	
400 405 410	
agc aag ctc acc gtg gac aag agc agg tgg cag cag ggg aac gtc ttc	1406

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
 415 420 425

tca tgc tcc gtg atg cat gag gct ctg cac aac cac tac acg cag aag 1454
 Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 430 435 440

agc ctc tcc ctg tct ccg ggt aaa tgagtgccac ggccggcaag ccccgctcc 1508
 Ser Leu Ser Leu Ser Pro Gly Lys
 445 450

ccaggctctc ggggtcgcgt gaggatgctt ggcacgtacc ccgtgtacat acttcccagg 1568
 caccagcat ggaaataaag caccagcgc tgccctggaa aaaaaaaaa 1616

<210> 28

<211> 470

<212> PRT

<213> Homo sapiens

<400> 28

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
 1 5 10 15
 Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
 20 25 30
 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 35 40 45
 Thr Gly Tyr Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
 50 55 60
 Glu Trp Met Gly Trp Ile Asn Pro His Ser Gly Gly Thr Asn Tyr Ala
 65 70 75 80
 Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser
 85 90 95
 Thr Ala Tyr Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val
 100 105 110
 Tyr Tyr Cys Ala Arg Thr Tyr Tyr Asp Ser Ser Gly Tyr Tyr His
 115 120 125
 Asp Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
 130 135 140
 Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
 145 150 155 160
 Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
 165 170 175
 Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
 180 185 190
 Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
 195 200 205
 Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr
 210 215 220
 Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
 225 230 235 240
 Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro
 245 250 255
 Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
 260 265 270
 Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
 275 280 285
 Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly

290	295	300
Val Glu Val His Asn Ala	Lys Thr Lys Pro Arg	Glu Glu Gln Phe Asn
305	310	315
Ser Thr Phe Arg Val Val	Ser Val Leu Thr Val	Val His Gln Asp Trp
	325	330
Leu Asn Gly Lys Glu Tyr	Lys Cys Lys Val	Ser Asn Lys Gly Leu Pro
	340	345
Ala Pro Ile Glu Lys Thr	Ile Ser Lys Thr	Lys Gly Gln Pro Arg Glu
	355	360
Pro Gln Val Tyr Thr Leu	Pro Pro Ser Arg	Glu Glu Met Thr Lys Asn
	370	375
Gln Val Ser Leu Thr Cys	Leu Val Lys Gly	Phe Tyr Pro Ser Asp Ile
385	390	395
Ala Val Glu Trp Glu Ser	Asn Gly Gln Pro	Glu Asn Asn Tyr Lys Thr
	405	410
Thr Pro Pro Met Leu Asp	Ser Asp Gly Ser	Phe Phe Leu Tyr Ser Lys
	420	425
Leu Thr Val Asp Lys Ser	Arg Trp Gln Gln	Gly Asn Val Phe Ser Cys
	435	440
Ser Val Met His Glu Ala	Leu His Asn His	Tyr Thr Gln Lys Ser Leu
	450	455
Ser Leu Ser Pro Gly Lys		460
465	470	

<210> 29

<211> 974

<212> DNA

<213> Homo sapiens

<220>

<221> 5'UTR

<222> (1)...(38)

<221> CDS

<222> (39)...(746)

<221> 3'UTR

<222> (750)...(974)

<221> sig_peptide

<222> (39)...(104)

<400> 29

gaattcgag tgccatgaca ccacgggcag gacacagc atg gac atg agg gtc ccc	56
Met Asp Met Arg Val Pro	
-20	

gct cag ctc ctg ggg ctc ctg ctg ctc tgg ttc cca ggt tcc aga tgc	104
Ala Gln Leu Leu Gly Leu Leu Leu Trp Phe Pro Gly Ser Arg Cys	
-15 -10 -5	

gac atc cag atg acc cag tct cca tct tcc gtg tct gca tct gta gga	152
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly	
1 5 10 15	

gac aga gtc acc atc act tgt cgg gcg agt cag ggt att agc agg ttg	200
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Arg Leu	

20	25	30	
tta gcc tgg tat cag cag aaa cca ggg aaa gcc cct aaa ctg atc			248
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile			
35	40	45	
tat gtt gca tcc agt ttg caa agt ggg gtc cca tca agg ttc agc ggc			296
Tyr Val Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly			
50	55	60	
agt gga tct ggg aca gat ttc act ctg acc atc agc agc ctg cag cct			344
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro			
65	70	75	80
gaa gat ttt gca act tac tat tgt caa cag gct aac agt ttc ccg tgg			392
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Phe Pro Trp			
85	90	95	
acg ttc ggc caa ggg acc aag gtg gaa atc aaa cga act gtg gct gca			440
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala			
100	105	110	
cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa tct gga			488
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly			
115	120	125	
act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga gag gcc			536
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala			
130	135	140	
aaa gta cag tgg aag gtg gat aac gcc ctg caa tcg ggt aac tcc cag			584
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln			
145	150	155	160
gag agt gtc aca gag cag gac agc aag gac agc acc tac agc ctg agc			632
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser			
165	170	175	
agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa gtc tac			680
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr			
180	185	190	
gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca aag agc			728
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser			
195	200	205	
ttc aac agg gga gag tgt tagagggaga agtgccccca cctgctctc			776
Phe Asn Arg Gly Glu Cys			
210			
agttccagcc tgacccccctc ccatacctttg gcctctgacc ctttttccac aggggacctta			836
ccctatttgc ggtcctccag ctcatctttc acctcaccac cctcctcctc cttggcttta			896
attatgctaa tgttgaggga gaatgaataa ataaagtga tctttgcaaa aaaaaaaaaa			956
aaaaatctct gcggccgc			974

<210> 30

<211> 236

<212> PRT

<213> Homo sapiens

<400> 30

```

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
 1           5           10           15
Phe Pro Gly Ser Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
 20           25           30
Val Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
 35           40           45
Gln Gly Ile Ser Arg Leu Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
 50           55           60
Ala Pro Lys Leu Leu Ile Tyr Val Ala Ser Ser Leu Gln Ser Gly Val
 65           70           75           80
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 85           90           95
Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
 100          105          110
Ala Asn Ser Phe Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
 115          120          125
Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
 130          135          140
Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
 145          150          155          160
Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
 165          170          175
Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
 180          185          190
Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
 195          200          205
Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
 210          215          220
Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 225          230          235

```

<210> 31

<211> 1708

<212> DNA

<213> Homo sapiens

<220>

<221> 5'UTR

<222> (1)...(93)

<221> CDS

<222> (94)...(1503)

<221> 3'UTR

<222> (1507)...(1708)

<221> sig_peptide

<222> (94)...(150)

<221> misc_feature

<222> (1)...(1708)

<223> n = A,T,C or G

<400> 31

```
gaattcgcag taccatgaca ccacgggagc ccagccttg ggattcccaa gtgtttgtaa      60
tcagtgatca ggactgagca cacaggactc acc atg gag ttg ggg ctg agc tgg      114
                               Met Glu Leu Gly Leu Ser Trp
                               -15
```

ggt ttc ctt gtt gct ata tta gaa ggt gtc cag tgt gag gtg cag ctg 162
Val Phe Leu Val Ala Ile Leu Glu Gly Val Gln Cys Glu Val Gln Leu
-10 -5 1

gtg	gag	tct	ggg	gga	ggc	ttg	gta	cag	cct	ggg	ggg	tcc	ctg	aga	ctc	210
Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly	Ser	Leu	Arg	Leu	
5					10					15					20	

tcc tgt gca gcc tct gga ttc acc ttc agt agc tac gac atg cac tgg 258
Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Asp Met His Trp
25 30 35

gtc cgc caa gct aca gga aaa ggt ctg gag tgg gtc tca gct att ggt 306
Val Arg Gln Ala Thr Gly Lys Gly Leu Glu Trp Val Ser Ala Ile Gly
40 45 50

act gct ggt gac aca tac tat cca ggc tcc gtg aag ggc cga ttc acc 354
Thr Ala Gly Asp Thr Tyr Tyr Pro Gly Ser Val Lys Gly Arg Phe Thr
55 60 65

```

atc tcc aga gaa aat gcc aag aac tcc ttg tat ctt caa atg aac agc      402
Ile Ser Arg Glu Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser
      70                      75                      80

```

```

ctg aga gcc ggg gac acg gct gtg tat tac tgt gta aga gat aat agg      450
Leu Arg Ala Gly Asp Thr Ala Val Tyr Tyr Cys Val Arg Asp Asn Arg
      85                      90                      95                      100

```

aag gtg acc cac gag cac tac tac tac tac ggt atg gac gtc tgg ggc 498
Lys Val Thr His Glu His Tyr Tyr Tyr Tyr Gly Met Asp Val Trp Gly
105 110 115

caa ggg acc acg gtc acc gtc tcc tca gcc tcc acc aag ggc cca tcg 546
Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
120 125 130

gtc ttc ccc ctg gcg ccc tgc tcc agg agc acc tcc gag agc aca gcg 594
Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala
135 140 145

gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg 642
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
150 155 160

tcg tgg aac tca ggc gct ctg acc agc ggc gtg cac acc ttc cca gct 690
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175 180

gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg 738
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
185 190 195

ccc tcc agc aac ttc ggc acc cag acc tac acc tgc aac gta gat cac	786
Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His	
200 205 210	
aag ccc agc aac acc aag gtg gac aag aca gtt gag cgc aaa tgt tgt	834
Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys	
215 220 225	
gtc gag tgc cca ccg tgc cca gca cca cct gtg gca gga ccg tca gtc	882
Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val	
230 235 240	
ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg acc	930
Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr	
245 250 255 260	
cct gag gtc acg tgc gtg gtg gtg gac gtg agc cac gaa gac ccc gag	978
Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu	
265 270 275	
gtc cag ttc aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag	1026
Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys	
280 285 290	
aca aag cca cgg gag gag cag ttc aac agc acg ttc cgt gtg gtc agc	1074
Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser	
295 300 305	
gtc ctc acc gtt gtg cac cag gac tgg ctg aac ggc aag gag tac aag	1122
Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys	
310 315 320	
tgc aag gtc tcc aac aaa ggc ctc cca gcc ccc atc gag aaa acc atc	1170
Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile	
325 330 335 340	
tcc aaa acc aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc	1218
Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro	
345 350 355	
cca tcc cgg gag gag atg acc aag aac cag gtc agc ctg acc tgc ctg	1266
Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu	
360 365 370	
gtc aaa ggc ttc tac ccc agc gac atc gcc gtg gag tgg gag agc aat	1314
Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn	
375 380 385	
ggg cag ccg gag aac aac tac aag acc aca cct ccc atg ctg gac tcc	1362
Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser	
390 395 400	
gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg gac aag agc agg	1410
Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg	
405 410 415 420	

tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg 1458
 Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
 425 430 435

cac aac cac tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa 1503
 His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 440 445 450

tgagtgccac ggccggcaag cccccgctcc ccaggctctc ggggtcgcgt gaggatgctt 1563
 ggcacgtacc ccgtgtacat acttcccagg caccacagcat ggaaataaag caccacgcgc 1623
 tgccctgggc ccttgcnaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1683
 aaaaaaaaaa aatctctgcg gccgc 1708

<210> 32

<211> 470

<212> PRT

<213> Homo sapiens

<400> 32

Met Glu Leu Gly Leu Ser Trp Val Phe Leu Val Ala Ile Leu Glu Gly
 1 5 10 15
 Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
 20 25 30
 Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
 35 40 45
 Ser Ser Tyr Asp Met His Trp Val Arg Gln Ala Thr Gly Lys Gly Leu
 50 55 60
 Glu Trp Val Ser Ala Ile Gly Thr Ala Gly Asp Thr Tyr Tyr Pro Gly
 65 70 75 80
 Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Ala Lys Asn Ser
 85 90 95
 Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Val Tyr
 100 105 110
 Tyr Cys Val Arg Asp Asn Arg Lys Val Thr His Glu His Tyr Tyr Tyr
 115 120 125
 Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 130 135 140
 Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
 145 150 155 160
 Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
 165 170 175
 Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
 180 185 190
 Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
 195 200 205
 Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr
 210 215 220
 Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
 225 230 235 240
 Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro
 245 250 255
 Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
 260 265 270
 Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
 275 280 285
 Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly
 290 295 300


```

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn
305          310          315          320
Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp
          325          330          335
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
          340          345          350
Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu
          355          360          365
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
          370          375          380
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
385          390          395          400
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
          405          410          415
Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
          420          425          430
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
          435          440          445
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
          450          455          460
Ser Leu Ser Pro Gly Lys
465          470

```

```

<210> 33
<211> 948
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> 5'UTR
<222> (1)...(27)

<221> CDS
<222> (28)...(735)

```

```

<221> 3'UTR
<222> (739)...(948)

```

```

<221> sig_peptide
<222> (28)...(87)

```

```

<221> misc_feature
<222> (1)...(948)
<223> n = A,T,C or G

```

```

<400> 33
gaattcgag tgccatgaca ccacgcc atg gaa acc cca gcg cag ctt ctc ttc      54
          Met Glu Thr Pro Ala Gln Leu Leu Phe
          -20          -15

```

```

ctc ctg cta ctc tgg ctc cca gat acc acc gga gaa att gtg ttg acg      102
Leu Leu Leu Leu Trp Leu Pro Asp Thr Thr Gly Glu Ile Val Leu Thr
          -10          -5          1          5

```

```

cag tct cca ggc acc ctg tct ttg tct cca ggg gaa aga gcc acc ctc      150
Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu
          10          15          20

```

tcc tgc agg gcc agt cag aat att aga agc agc tac tta gcc tgg tac	198
Ser Cys Arg Ala Ser Gln Asn Ile Arg Ser Ser Tyr Leu Ala Trp Tyr	
25 30 35	
cag cag aaa cct ggc cag gct ccc ggg ctc ctc atc tat ggt gca tcc	246
Gln Gln Lys Pro Gly Gln Ala Pro Gly Leu Leu Ile Tyr Gly Ala Ser	
40 45 50	
agc agg gcc act ggc atc cca gac agg ttc agt ggc agt ggg tct ggg	294
Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly	
55 60 65	
aca gac ttc act ctc acc atc agc aga ctg gag cct gaa gat ttt gca	342
Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala	
70 75 80 85	
gtg tat tac tgt cag cag ttt ggt agc tca cct atg tgc agt ttt ggc	390
Val Tyr Tyr Cys Gln Gln Phe Gly Ser Phe Pro Met Cys Ser Phe Gly	
90 95 100	
cag ggg acc aag ctg gag atc aaa cga act gtg gct gca cca tct gtc	438
Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val	
105 110 115	
ttc atc ttc ccg cca tct gat gag cag ttg aaa tct gga act gcc tct	486
Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser	
120 125 130	
gtt gtg tgc ctg ctg aat aac ttc tat ccc aga gag gcc aaa gta cag	534
Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln	
135 140 145	
tgg aag gtg gat aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc	582
Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val	
150 155 160 165	
aca gag cag gac agc aag gac agc acc tac agc ctc agc agc acc ctg	630
Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu	
170 175 180	
acg ctg agc aaa gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa	678
Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu	
185 190 195	
gtc acc cat cag ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg	726
Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg	
200 205 210	
gga gag tgt tagagggaga antgccccca cctgctcctc agttccagcc	775
Gly Glu Cys	
215	
tgacccccctc ccatacctttg gcctctgacc cttttttccac aggggaccta cccctattgc	835
ggtcctccag ctcatctttc acctcaccac cctcctcctc cttggcttta attatgctaa	895
tgttgaggga gaatgaataa ataaagtga tctttgcacc tgtgaaaaaa aaa	948

<210> 34
 <211> 236
 <212> PRT
 <213> Homo sapiens

<400> 34
 Met Glu Thr Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
 1 5 10 15
 Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser
 20 25 30
 Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Asn
 35 40 45
 Ile Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala
 50 55 60
 Pro Gly Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro
 65 70 75 80
 Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
 85 90 95
 Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Phe
 100 105 110
 Gly Ser Ser Pro Met Cys Ser Phe Gly Gln Gly Thr Lys Leu Glu Ile
 115 120 125
 Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
 130 135 140
 Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
 145 150 155 160
 Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
 165 170 175
 Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
 180 185 190
 Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
 195 200 205
 Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
 210 215 220
 Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 225 230 235

<210> 35
 <211> 1673
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> (1)...(95)

<221> CDS
 <222> (96)...(1505)

<221> 3'UTR
 <222> (1509)...(1673)

<221> sig_peptide
 <222> (96)...(152)

<400> 35
 gaattcgag tgccatgaca ccacggtgga gccccagcct tgggattccc aagtgtttgt 60

attcagtgat caggactgaa cacacaggac tcacc atg gag ttg ggg ctg agc	113
Met Glu Leu Gly Leu Ser	
-15	
tggtgtttttcttggtgctatatta gaa ggt gtc cag tgt gag gtg cag	161
Trp Val Phe Leu Val Ala Ile Leu Glu Gly Val Gln Cys Glu Val Gln	
-10 -5 1	
ctg gtg gag tct ggg gga ggc ttg gta cag cct ggg ggg tcc ctg aga	209
Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg	
5 10 15	
ctc tcc tgt gca gcc tct gga ttc acc ttc agt agc tac gac atg cac	257
Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Asp Met His	
20 25 30 35	
tggtgtc cgc caa gct aca gga aaa ggt ctg gag tgg gtc tca gct att	305
Trp Val Arg Gln Ala Thr Gly Lys Gly Leu Glu Trp Val Ser Ala Ile	
40 45 50	
ggt act gct ggt gac aca tac tat cca ggc tcc gtg aag ggc cga ttc	353
Gly Thr Ala Gly Asp Thr Tyr Tyr Pro Gly Ser Val Lys Gly Arg Phe	
55 60 65	
acc atc tcc aga gaa aat gcc aag aac tcc ttg tat ctt caa atg aac	401
Thr Ile Ser Arg Glu Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn	
70 75 80	
agc ctg aga gcc ggg gac acg gct gtg tat tac tgt gta aga gat aag	449
Ser Leu Arg Ala Gly Asp Thr Ala Val Tyr Tyr Cys Val Arg Asp Lys	
85 90 95	
agg acg gtg acc cac gag cac tac tac tac tac ggt atg gac gtc tgg	497
Arg Thr Val Thr His Glu His Tyr Tyr Tyr Tyr Gly Met Asp Val Trp	
100 105 110 115	
ggc caa ggg acc acg gtc acc gtc tcc tca gcc tcc acc aag ggc cca	545
Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro	
120 125 130	
tcg gtc ttc ccc ctg gcg ccc tgc tcc agg agc acc tcc gag agc aca	593
Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr	
135 140 145	
gcg gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acc	641
Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr	
150 155 160	
gtg tcg tgg aac tca ggc gct ctg acc agc ggc gtg cac acc ttc cca	689
Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro	
165 170 175	
gct gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc	737
Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr	
180 185 190 195	
gtg ccc tcc agc aac ttc ggc acc cag acc tac acc tgc aac gta gat	785

Val	Pro	Ser	Ser	Asn	Phe	Gly	Thr	Gln	Thr	Tyr	Thr	Cys	Asn	Val	Asp		
				200					205					210			
cac	aag	ccc	agc	aac	acc	aag	gtg	gac	aag	aca	gtt	gag	cgc	aaa	tgt	833	
His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Thr	Val	Glu	Arg	Lys	Cys		
			215					220					225				
tgt	gtc	gag	tgc	cca	ccg	tgc	cca	gca	cca	cct	gtg	gca	gga	ccg	tca	881	
Cys	Val	Glu	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Pro	Val	Ala	Gly	Pro	Ser		
		230						235				240					
gtc	ttc	ctc	ttc	ccc	cca	aaa	ccc	aag	gac	acc	ctc	atg	atc	tcc	cgg	929	
Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg		
	245						250				255						
acc	cct	gag	gtc	acg	tgc	gtg	gtg	gtg	gac	gtg	agc	cac	gaa	gac	ccc	977	
Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro		
260					265				270					275			
gag	gtc	cag	ttc	aac	tgg	tac	gtg	gac	ggc	gtg	gag	gtg	cat	aat	gcc	1025	
Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala		
				280					285					290			
aag	aca	aag	cca	cgg	gag	gag	cag	ttc	aac	agc	acg	ttc	cgt	gtg	gtc	1073	
Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Phe	Arg	Val	Val		
			295					300					305				
agc	gtc	ctc	acc	gtt	gtg	cac	cag	gac	tgg	ctg	aac	ggc	aag	gag	tac	1121	
Ser	Val	Leu	Thr	Val	Val	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr		
		310					315					320					
aag	tgc	aag	gtc	tcc	aac	aaa	ggc	ctc	cca	gcc	ccc	atc	gag	aaa	acc	1169	
Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr		
	325					330					335						
atc	tcc	aaa	acc	aaa	ggg	cag	ccc	cga	gaa	cca	cag	gtg	tac	acc	ctg	1217	
Ile	Ser	Lys	Thr	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu		
340					345				350					355			
ccc	cca	tcc	cgg	gag	gag	atg	acc	aag	aac	cag	gtc	agc	ctg	acc	tgc	1265	
Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys		
			360						365				370				
ctg	gtc	aaa	ggc	ttc	tac	ccc	agc	gac	atc	gcc	gtg	gag	tgg	gag	agc	1313	
Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser		
			375					380					385				
aat	ggg	cag	ccg	gag	aac	aac	tac	aag	acc	aca	cct	ccc	atg	ctg	gac	1361	
Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Met	Leu	Asp		
		390					395					400					
tcc	gac	ggc	tcc	ttc	ttc	ctc	tac	agc	aag	ctc	acc	gtg	gac	aag	agc	1409	
Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser		
	405					410					415						
agg	tgg	cag	cag	ggg	aac	gtc	ttc	tca	tgc	tcc	gtg	atg	cat	gag	gct	1457	
Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala		

```
<210> 36
<211> 470
<212> PRT
<213> Homo sapiens
```

<400>	36														
Met	Glu	Leu	Gly	Leu	Ser	Trp	Val	Phe	Leu	Val	Ala	Ile	Leu	Glu	Gly
1				5					10					15	
Val	Gln	Cys	Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln
			20					25					30		
Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe
		35				40						45			
Ser	Ser	Tyr	Asp	Met	His	Trp	Val	Arg	Gln	Ala	Thr	Gly	Lys	Gly	Leu
	50					55					60				
Glu	Trp	Val	Ser	Ala	Ile	Gly	Thr	Ala	Gly	Asp	Thr	Tyr	Tyr	Pro	Gly
65					70					75					80
Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Glu	Asn	Ala	Lys	Asn	Ser
				85					90					95	
Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Gly	Asp	Thr	Ala	Val	Tyr
			100					105					110		
Tyr	Cys	Val	Arg	Asp	Lys	Arg	Thr	Val	Thr	His	Glu	His	Tyr	Tyr	Tyr
		115					120					125			
Tyr	Gly	Met	Asp	Val	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser
	130					135					140				
Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg
145					150					155					160
Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr
				165					170					175	
Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser
			180					185					190		
Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser
		195					200					205			
Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Asn	Phe	Thr	Gln	Thr	
	210					215					220				
Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys
225					230					235					240
Thr	Val	Glu	Arg	Lys	Cys	Cys	Val	Glu	Cys	Pro	Pro	Cys	Pro	Ala	Pro
				245					250					255	
Pro	Val	Ala	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp
			260					265					270		
Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp
		275					280					285			
Val	Ser	His	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly
	290					295				300					
Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn
305					310					315					320
Ser	Thr	Phe	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Val	His	Gln	Asp	Trp

```

          325          330          335
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
          340          345          350
Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu
          355          360          365
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
          370          375          380
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
          385          390          395          400
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
          405          410          415
Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
          420          425          430
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
          435          440          445
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
          450          455          460
Ser Leu Ser Pro Gly Lys
          465          470

```

```

<210> 37
<211> 970
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> 5'UTR
<222> (1)...(32)

```

```

<221> CDS
<222> (33)...(740)

```

```

<221> 3'UTR
<222> (744)...(970)

```

```

<221> sig_peptide
<222> (33)...(92)

```

```

<400> 37
gaattgcgag tgccatgaca ccacggggaa cc atg gaa acc cca gcg cag ctt      53
                               Met Glu Thr Pro Ala Gln Leu
                               -20          -15

ctc ttc ctc ctg cta ctc tgg ctc cca gat acc acc gga gaa att gtg      101
Leu Phe Leu Leu Leu Leu Trp Leu Pro Asp Thr Thr Gly Glu Ile Val
          -10          -5          1

ttg acg cag tct cca ggc acc ctg tct ttg tct cca ggg gaa aga gcc      149
Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala
          5          10          15

acc ctc tcc tgc agg gcc agt cag agt att agc agc agc tcc tta gcc      197
Thr Leu Ser Cys Arg Ala Ser Gln Ser Ile Ser Ser Ser Ser Leu Ala
          20          25          30          35

tgg tac cag cag aaa cct ggc cag gct ccc ggg ctc ctc atc ttt ggt      245
Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Gly Leu Leu Ile Phe Gly

```

40	45	50	
gca tcc agc agg gcc act ggc atc cca gac agg ttc agt ggc agt ggg			293
Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly			
55	60	65	
tct ggg aca gac ttc act ctc acc atc agc aga ctg gag cct gaa gat			341
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp			
70	75	80	
ttt gca gtg tat tac tgt cag cag ttt ggt agc tca cct atg tgc agt			389
Phe Ala Val Tyr Tyr Cys Gln Gln Phe Gly Ser Ser Pro Met Cys Ser			
85	90	95	
ttt ggc cag ggg acc aag ctg gag atc aaa cga act gtg gct gca cca			437
Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala Pro			
100	105	110	115
tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa tct gga act			485
Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr			
120	125	130	
gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga gag gcc aaa			533
Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys			
135	140	145	
gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac tcc cag gag			581
Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu			
150	155	160	
agt gtc aca gag cag gac agc aag gac agc acc tac agc ctc agc agc			629
Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser			
165	170	175	
acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa gtc tac gcc			677
Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala			
180	185	190	195
tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca aag agc ttc			725
Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe			
200	205	210	
aac agg gga gag tgt tagagggaga agtgcccca cctgctcctc agttccagcc			780
Asn Arg Gly Glu Cys			
215			
tgacccccctc ccatacctttg gcctctgacc ctttttccac aggggaccta cccctattgc			840
ggtcctccag ctcactctttc acctcacccc cctcctcctc cttggcttta attatgctaa			900
tgttgaggga gaatgaataa ataaagtga tctttgcaaa aaaaaaaaaa aaaaaaatct			960
ctcgggccgc			970

<210> 38

<211> 236

<212> PRT

<213> Homo sapiens

<400> 38


```

Met Glu Thr Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
 1          5          10          15
Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser
          20          25          30
Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
          35          40          45
Ile Ser Ser Ser Ser Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala
          50          55          60
Pro Gly Leu Leu Ile Phe Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro
          65          70          75          80
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
          85          90          95
Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Phe
          100          105          110
Gly Ser Ser Pro Met Cys Ser Phe Gly Gln Gly Thr Lys Leu Glu Ile
          115          120          125
Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
          130          135          140
Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
          145          150          155          160
Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
          165          170          175
Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
          180          185          190
Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
          195          200          205
Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
          210          215          220
Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
          225          230          235

```

<210> 39

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Artificially synthesized primer sequence

<221> primer_bind

<222> (1)...(35)

<400> 39

gaggtctccg ccctcgagat gcggctgggc agtcc

35

<210> 40

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Artificially synthesized primer sequence

<221> primer_bind

<222> (1)...(33)

<400> 40

cacaggacag ccaggggatc ccacgtggcc gcg

33

<210> 41

<211> 6

<212> PRT

<213> Homo sapiens

<400> 41

Met Tyr Pro Pro Pro Tyr

1

5

<210> 42

<211> 4

<212> PRT

<213> Homo sapiens

<400> 42

Tyr Met Asn Met

1

<210> 43

<211> 4

<212> PRT

<213> Homo sapiens

<400> 43

Tyr Val Lys Met

1